57. (New) The polypeptide of claim 56, wherein the amino acid sequence of said polypeptide comprises a conservative amino acid substitution relative to the amino acid sequence of SEQ ID NO:4.

58. (New) The polypeptide of claim 56, wherein the amino acid sequence of said polypeptide comprises a nonconservative amino acid substitution relative to the amino acid sequence of SEQ ID NO:4.

59. (New) The polypeptide of claim 2, wherein the amino acid sequence is a naturally-occurring allelic variant of SEQ ID NO:4.

60. (New) An isolated polypeptide comprising the amino acid sequence of a mature form of SEQ ID NO:4.

61. (New) An isolated polypeptide comprising the amino acid sequence of a variant of a mature form of SEQ ID NO:4.

62. (New) The polypeptide of claim 61, wherein no more than 10% of the amino acid residues of said polypeptide differ from the amino acid sequence of the mature form of SEQ ID NO:4.

63. (New) The polypeptide of claim 62, wherein the amino acid sequence of said polypeptide comprises a conservative amino acid substitution relative to the amino acid sequence of the mature form of SEQ ID NO:4.

64. (New) The polypeptide of claim 62, wherein the amino acid sequence of said polypeptide comprises a nonconservative amino acid substitution relative to the amino acid sequence of the mature form of SEQ ID NO:4.

65. (New) The polypeptide of claim 61, wherein the amino acid sequence is a naturally-occurring allelic variant of a mature form of SEQ ID NO:4.

66. (New) An isolated polypeptide consisting essentially of the amino acid sequence of SEQ ID NO:4.

B2

67. (New) An isolated polypeptide consisting of the amino acid sequence of SEQ ID NO:4.

68. (New) The polypeptide of claim 1, wherein said polypeptide is recombinantly produced.

In the Specification:

Replace the paragraph starting on page 3, line 29 with the following:

B3

The invention is based in part on the discovery of novel nucleic acids encoding a novel human transmembrane protein (NOVTRAN), a neuromedin peptide (NOVNEUR), a gonadotropin-like protein (NOVGON), and three interleukin-1 receptor antagonist proteins (NOVINTRA A, B, and C), hereinafter collectively referred to as "NOVX" polypeptides or nucleic acids.

Replace the paragraph starting on page 4, line 4 with the following:

B4

In one aspect, the invention provides isolated nucleic acid sequences encoding novel NOVTRAN, NOVNEUR, NOVGON, NOVINTRA A, and NOVINTRA B and NOVINTRA C polypeptides, wherein the nucleic acid sequences is selected from SEQ ID NOs: 1, 3, 5, 7, 9, and 11, respectively, or an allelic or substitution variant thereof. In another aspect, there is provided an oligonucleotide that includes a portion of a NOVX nucleic acid sequence, *e.g.* SEQ ID NOs: 1, 3, 5, 7, 9, and 11, respectively.

Replace the paragraph starting on page 4, line 22 with the following:

B5

In another aspect, there is provided an isolated NOVTRAN, NOVNEUR, NOVGON, NOVINTRA A, and NOVINTRA B, and NOVINTRA C polypeptide encoded by an isolated nucleic acid sequence or oligonucleotide described herein. In some aspects, the isolated NOVX protein comprises an amino acid sequence selected from SEQ ID NOs: 2, 4, 6, 8, 10, or 12, respectively, or functional variants or fragments thereof. In another embodiment, a variant or fragment of a NOVX protein retains the respective NOVX-like protein activity.

Replace the paragraph starting on page 10, line 8 with the following:

A novel human transmembrane protein (NOVTRAN) gene was identified based on its homology to human chromosome 22 exon mRNA (acc: H55724) (see Fig. 2A). Protein sorting prediction analysis (PSORT) revealed that this sequence localized to the plasma membrane protein (certainty = 0.6500), the mitochondrial inner membrane (certainty = 0.5638), mitochondrial matrix (certainty = 0.3572) and/or intermembrane space (certainty = 0.3572). Sequence analysis of the genomic DNA fragment AC007663_A generated an extended, predicted cDNA of 1047 nucleotides (Figure 1A; start/stop codons shown in bold). The amino acid sequence encoded by the cDNA is not similar to any known proteins (see Figures 1B and 2B). The NOVTRAN nucleic acid sequence of the invention is shown in Fig. 1A. The disclosed nucleotide sequence encodes a NOVTRAN protein of 348 amino acids (SEQ ID NO: 2; also shown in Fig. 1B). This sequence contains a likely signal peptide cleavage site between amino acids residues 19 and 20 (VLS-LL) of SEQ ID NO: 1B.

B6

Replace the paragraph starting on page 12, line 5 with the following:

A novel human gonadotropin-like (NOVGON) gene was identified based on its homology to *Salmo salar* gonadotropin II beta subunit mRNA (GII-B) (acc: AF146151) (see Fig. 7A). Sequence analysis of the genomic DNA fragment AL49871 generated a cDNA of 693 nucleotides (Figure 6A). The amino acid sequence encoded by the cDNA is 43% identical and 61% similar to a 144 amino acid *Cyprinus carpio* (common carp) gonadotropin beta chain precursor (SwissProt acc: P01235) (see Figures 6B and 7B). PSORT analysis confirmed this sequence is cytoplasmic protein (certainty = 0.7953), possibly also localized to lysozyme lumen (certainty = 0.4242). The NOVGON nucleic acid sequence of the invention is shown in Fig. 6A. The disclosed sequence is 693 nucleotides in length (SEQ ID NO:5), and encodes a NOVGON protein of 230 amino acids (SEQ ID NO:6; also shown in Fig. 6B). Hydrophobicity analysis of the amino acid sequence indicates that NOVGON is largely hydrophilic, having a distinct hydrophobic domain at its N-terminus, a somewhat hydrophobic domain near its C-terminus. *See* Fig. 20.

B7

Replace the paragraph starting on page 13, line 9 with the following:

B8 Three novel human interleukin-1 receptor antagonist-like (NOVINTRA) genes were identified based on their homology to *Equus callabrus* antagonist secretory form (IL-1ra) gene (acc: AF072476) or *Sus scrofa* IRAP1 mRNA (acc: L38849), respectively (*see* Figs. 10A, 13A, and 16A, respectively).

Replace the paragraph starting on page 14, line 10 with the following:

B9 Sequence analysis of the genomic DNA fragment AC016724_B generated a cDNA of 520 nucleotides (Figure 12A) containing a 170 amino acid coding sequence (stop/start codons shown in bold in Fig. 12A). The amino acid sequence encoded by the cDNA is 100% identical to a 157 amino acid FIL-1 ETA protein (Sptrembl-acc: Q9UHA5; *see* Smith *et al., supra.*), and 94% identical and 95% positive to a 164 amino acid human interleukin-1 homolog 2 protein (Sptrembl-acc: Q9NZH7; Kumar *et al., J. Biol. Chem. 275:* 10308-314 (2000)) (*see* Figs. 12A and 13B). NOVINTRA A is also 35% identical and 51% similar to a 155 amino acid human IL 1RN homolog (Tremblnew acc: AAF02757) (*see* Fig. 13B). PSORT analysis confirmed this sequence is a microbody (peroxisome) protein (certainty = 0.5035), possibly also localized to the cytoplasm (certainty = 0.4500). The NOVINTRA B nucleic acid sequence of the invention is shown in Fig. 12A. The disclosed sequence is 520 nucleotides in length (SEQ ID NO: 9), and contains a 7 nucleotide putative UTR (residues 514 to 520 of SEQ ID NO: 9). The coding sequence encodes a NOVINTRA B protein of 170 amino acids (SEQ ID NO: 10; also shown in Fig. 12B). Hydrophobicity analysis of the amino acid sequence indicates that NOVINTRA B contains two distinct hydrophobic domains, one near its N-terminus, and the other in the middle of the protein, and has a largely hydrophilic C-terminus. *See* Fig. 22.

Replace the paragraph starting on page 16, line 12 with the following:

B10 A NOVINTRA polypeptide, *e.g.* NOVINTRA A, B, or C, of the invention encompasses a protein described herein, or mature forms arising therefrom as a result of post-translational modifications. Thus, the proteins of the invention encompass both a precursor and any active forms of the NOVINTRA proteins.